

## SEQUENCE LISTING

<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

<120> GLUTAMINE:FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE (GFAT) COMPRISING AN INTERNAL PURIFICATION TAG, AND ITS USE FOR THE SCREENING OF COMPOUNDS

<130> WOB 03 BP CNR GFAT

<160> 19

<170> PatentIn version 3.1

<210> 1

<211> 2046

<212> DNA

<213> Homo sapiens

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<221> misc\_feature

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Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys	
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Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly	
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Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp	
85 90 95	
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Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser	
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 Val Phe Asn Thr Met Arg Gly Arg Val Asn Phe Glu Thr Asn Thr Val

340					345					350					
Leu	Leu	Gly	Gly	Leu	Lys	Asp	His	Leu	Lys	Glu	Ile	Arg	Arg	Cys	Arg
		355					360					365			
Arg	Leu	Ile	Val	Ile	Gly	Cys	Gly	Thr	Ser	Tyr	His	Ala	Ala	Val	Ala
	370					375					380				
Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr	Glu	Leu	Pro	Val	Met	Val	Glu
	385					390					395				400
Leu	Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn	Thr	Pro	Val	Phe	Arg	Asp	Asp
				405					410					415	
Val	Cys	Phe	Phe	Ile	Ser	Gln	Ser	Gly	Glu	Thr	Ala	Asp	Thr	Leu	Leu
			420					425					430		
Ala	Leu	Arg	Tyr	Cys	Lys	Asp	Arg	Gly	Ala	Leu	Thr	Val	Gly	Val	Thr
	435						440					445			
Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	Glu	Thr	Asp	Cys	Gly	Val	His
	450					455					460				
Ile	Asn	Ala	Gly	Pro	Glu	Val	Gly	Val	Ala	Ser	Thr	Lys	Ala	Tyr	Thr
	465					470					475				480
Ser	Gln	Phe	Ile	Ser	Leu	Val	Met	Phe	Gly	Leu	Met	Met	Ser	Glu	Asp
				485					490					495	
Arg	Ile	Ser	Leu	Gln	Asn	Arg	Arg	Gln	Glu	Ile	Ile	Arg	Gly	Leu	Arg
			500					505					510		
Ser	Leu	Pro	Glu	Leu	Ile	Lys	Glu	Val	Leu	Ser	Leu	Glu	Glu	Lys	Ile
		515					520					525			
His	Asp	Leu	Ala	Leu	Glu	Leu	Tyr	Thr	Gln	Arg	Ser	Leu	Leu	Val	Met
	530					535					540				
Gly	Arg	Gly	Tyr	Asn	Tyr	Ala	Thr	Cys	Leu	Glu	Gly	Ala	Leu	Lys	Ile
	545					550					555				560
Lys	Glu	Ile	Thr	Tyr	Met	His	Ser	Glu	Gly	Ile	Leu	Ala	Gly	Glu	Leu
				565					570					575	
Lys	His	Gly	Pro	Leu	Ala	Leu	Ile	Asp	Lys	Gln	Met	Pro	Val	Ile	Met
			580					585					590		
Val	Ile	Met	Lys	Asp	Pro	Cys	Phe	Ala	Lys	Cys	Gln	Asn	Ala	Leu	Gln
		595					600					605			
Gln	Val	Thr	Ala	Arg	Gln	Gly	Arg	Pro	Ile	Ile	Leu	Cys	Ser	Lys	Asp
	610					615					620				
Asp	Thr	Glu	Ser	Ser	Lys	Phe	Ala	Tyr	Lys	Thr	Ile	Glu	Leu	Pro	His
	625					630					635				640
Thr	Val	Asp	Cys	Leu	Gln	Gly	Ile	Leu	Ser	Val	Ile	Pro	Leu	Gln	Leu
				645					650					655	
Leu	Ser	Phe	His	Leu	Ala	Val	Leu	Arg	Gly	Tyr	Asp	Val	Asp	Phe	Pro

660

665

670

Arg Asn Leu Ala Lys Ser Val Thr Val Glu  
 675 680

<210> 5  
 <211> 2100  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(2100)  
 <223>

<220>  
 <221> misc\_feature  
 <222> (170)..(170)  
 <223> t or c

<400> 5  
 atg tgt ggt ata ttt gct tac tta aac tac cat gtt cct cga acg aga 48  
 Met Cys Gly Ile Phe Ala Tyr Leu Asn Tyr His Val Pro Arg Thr Arg  
 1 5 10 15

cga gaa atc ctg gag acc cta atc aaa ggc ctt cag aga ctg gag tac 96  
 Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr  
 20 25 30

aga gga tat gat tct gct ggt gtg gga ttt gat gga ggc aat gat aaa 144  
 Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys  
 35 40 45

gat tgg gaa gcc aat gcc tgc aaa anc cag ctt att aag aag aaa gga 192  
 Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly  
 50 55 60

aaa gtt aag gca ctg gat gaa gaa gtt cac aag caa caa gat atg gat 240  
 Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp  
 65 70 75 80

ttg gat ata gaa ttt gat gta cac ctt gga ata gct cat acc cgt tgg 288  
 Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp  
 85 90 95

gca aca cat gga gaa ccc agt cct gtc aat agc cac ccc cag cgc tct 336  
 Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser  
 100 105 110

gat aaa aat aat gaa ttt atc gtt att cac aat gga atc atc acc aac 384  
 Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn  
 115 120 125

tac aaa gac ttg aaa aag ttt ttg gaa agc aaa ggc tat gac ttc gaa 432  
 Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu  
 130 135 140

tct gaa aca gac aca gag aca att gcc aag ctc gtt aag tat atg tat 480

Ser 145	Glu	Thr	Asp	Thr	Glu 150	Thr	Ile	Ala	Lys	Leu 155	Val	Lys	Tyr	Met	Tyr 160	
gac Asp	aat Asn	cgg Arg	gaa Glu	agt Ser	caa Gln	gat Asp	acc Thr	agc Ser	ttt Phe	act Thr	acc Thr	ttg Leu	gtg Val	gag Glu	aga Arg	528
gtt Val	atc Ile	caa Gln	caa Gln	ttg Leu	gaa Glu	ggg Gly	gct Ala	ttt Phe	gca Ala	ctt Leu	gtg Val	ttt Phe	aaa Lys	agt Ser	gtt Val	576
cat His	ttt Phe	ccc Pro	ggg Gly	caa Gln	gca Ala	gtt Val	ggc Gly	aca Thr	agg Arg	cga Arg	ggg Gly	agc Ser	cct Pro	ctg Leu	ttg Leu	624
att Ile	ggg Gly	gta Val	cgg Arg	agt Ser	gaa Glu	cat His	aaa Lys	ctt Leu	tct Ser	act Thr	gat Asp	cac His	att Ile	cct Pro	ata Ile	672
ctc Leu	tac Tyr	aga Arg	aca Thr	gct Ala	agg Arg	act Thr	cag Gln	att Ile	gga Gly	tca Ser	aaa Lys	ttc Phe	aca Thr	cgg Arg	tgg Trp	720
gga Gly	tca Ser	cag Gln	gga Gly	gaa Glu	aga Arg	ggc Gly	aaa Lys	gac Asp	aag Lys	aaa Lys	gga Gly	agc Ser	tgc Cys	aat Asn	ctc Leu	768
tct Ser	cgt Arg	gtg Val	gac Asp	agc Ser	aca Thr	acc Thr	tgc Cys	ctt Leu	ttc Phe	ccg Pro	gtg Val	gaa Glu	gaa Glu	aaa Lys	gca Ala	816
gtg Val	gag Glu	tat Tyr	tac Tyr	ttt Phe	gct Ala	tct Ser	gat Asp	gca Ala	agt Ser	gct Ala	gtc Val	ata Ile	gaa Glu	cac His	acc Thr	864
aat Asn	cgc Arg	gtc Val	atc Ile	ttt Phe	ctg Leu	gaa Glu	gat Asp	gat Asp	gat Asp	gtt Val	gca Ala	gca Ala	gta Val	gtg Val	gat Asp	912
gga Gly	cgt Arg	ctt Leu	tct Ser	atc Ile	cat His	cga Arg	att Ile	aaa Lys	cga Arg	act Thr	gca Ala	gga Gly	gat Asp	cac His	ccc Pro	960
gga Gly	cga Arg	gct Ala	gtg Val	caa Gln	aca Thr	ctc Leu	cag Gln	atg Met	gaa Glu	ctc Leu	cag Gln	cag Gln	atc Ile	atg Met	aag Lys	1008
ggc Gly	aac Asn	ttc Phe	agt Ser	tca Ser	ttt Phe	atg Met	cag Gln	aag Lys	gaa Glu	ata Ile	ttt Phe	gag Glu	cag Gln	cca Pro	gag Glu	1056
tct Ser	gtc Val	gtg Val	aac Asn	aca Thr	atg Met	aga Arg	gga Gly	aga Arg	gtc Val	aac Asn	ttt Phe	gat Asp	gac Asp	tat Tyr	act Thr	1104
gtg Val	aat Asn	ttg Leu	ggg Gly	ggg Gly	ttg Leu	aag Lys	gat Asp	cac His	ata Ile	aag Lys	gag Glu	atc Ile	cag Gln	aga Arg	tgc Cys	1152
cgg Arg	cgt Arg	ttg Leu	att Ile	ctt Leu	att Ile	gct Ala	tgt Cys	gga Gly	aca Thr	agt Ser	tac Tyr	cat His	gct Ala	ggg Gly	gta Val	1200

385	390	395	400	
gca aca cgt caa gtt ctt gag gag ctg act gag ttg cct gtg atg gtg Ala Thr Arg Gln Val Leu Glu Glu Leu Thr Glu Leu Pro Val Met Val 405 410 415				1248
gaa cta gca agt gac ttc ctg gac aga aac aca cca gtc ttt cga gat Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro Val Phe Arg Asp 420 425 430				1296
gat gtt tgc ttt ttc ctt agt caa tca ggt gag aca gca gat act ttg Asp Val Cys Phe Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp Thr Leu 435 440 445				1344
atg ggt ctt cgt tac tgt aag gag aga gga gct tta act gtg ggg atc Met Gly Leu Arg Tyr Cys Lys Glu Arg Gly Ala Leu Thr Val Gly Ile 450 455 460				1392
aca aac aca gtt ggc agt tcc ata tca cgg gag aca gat tgt gga gtt Thr Asn Thr Val Gly Ser Ser Ile Ser Arg Glu Thr Asp Cys Gly Val 465 470 475 480				1440
cat att aat gct ggt cct gag att ggt gtg gcc agt aca aag gct tat His Ile Asn Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr 485 490 495				1488
acc agc cag ttt gta tcc ctt gtg atg ttt gcc ctt atg atg tgt gat Thr Ser Gln Phe Val Ser Leu Val Met Phe Ala Leu Met Met Cys Asp 500 505 510				1536
gat cgg atc tcc atg caa gaa aga cgc aaa gag atc atg ctt gga ttg Asp Arg Ile Ser Met Gln Glu Arg Arg Lys Glu Ile Met Leu Gly Leu 515 520 525				1584
aaa cgg ctg cct gat ttg att aag gaa gta ctg agc atg gat gac gaa Lys Arg Leu Pro Asp Leu Ile Lys Glu Val Leu Ser Met Asp Asp Glu 530 535 540				1632
att cag aaa cta gca aca gaa ctt tat cat cag aag tca gtt ctg ata Ile Gln Lys Leu Ala Thr Glu Leu Tyr His Gln Lys Ser Val Leu Ile 545 550 555 560				1680
atg gga cga ggc tat cat tat gct act tgt ctt gaa ggg gca ctg aaa Met Gly Arg Gly Tyr His Tyr Ala Thr Cys Leu Glu Gly Ala Leu Lys 565 570 575				1728
atc aaa gaa att act tat atg cac tct gaa ggc atc ctt gct ggt gaa Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly Ile Leu Ala Gly Glu 580 585 590				1776
ttg aaa cat ggc cct ctg gct ttg gtg gat aaa ttg atg cct gtg atc Leu Lys His Gly Pro Leu Ala Leu Val Asp Lys Leu Met Pro Val Ile 595 600 605				1824
atg atc atc atg aga gat cac act tat gcc aag tgt cag aat gct ctt Met Ile Ile Met Arg Asp His Thr Tyr Ala Lys Cys Gln Asn Ala Leu 610 615 620				1872
cag caa gtg gtt gct cgg cag ggg cgg cct gtg gta att tgt gat aag Gln Gln Val Val Ala Arg Gln Gly Arg Pro Val Val Ile Cys Asp Lys				1920

625	630	635	640	
gag gat act gag acc att aag aac aca aaa aga acg atc aag gtg ccc				1968
Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr Ile Lys Val Pro				
	645	650	655	
cac tca gtg gac tgc ttg cag ggc att ctc agc gtg atc cct tta cag				2016
His Ser Val Asp Cys Leu Gln Gly Ile Leu Ser Val Ile Pro Leu Gln				
	660	665	670	
ttg ctg gct ttc cac ctt gct gtg ctg aga ggc tat gat gtt gat ttc				2064
Leu Leu Ala Phe His Leu Ala Val Leu Arg Gly Tyr Asp Val Asp Phe				
	675	680	685	
cca cgg aat ctt gcc aaa tct gtg act gta gag tga				2100
Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu				
	690	695		

<210> 6  
 <211> 699  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <221> misc\_feature  
 <222> (57)..(57)  
 <223> 'Xaa' in position 57 represents Thr or Ile

<400> 6  
 Met Cys Gly Ile Phe Ala Tyr Leu Asn Tyr His Val Pro Arg Thr Arg  
 1 5 10 15  
  
 Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr  
 20 25 30  
  
 Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys  
 35 40 45  
  
 Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly  
 50 55 60  
  
 Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp  
 65 70 75 80  
  
 Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp  
 85 90 95  
  
 Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser  
 100 105 110  
  
 Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn  
 115 120 125  
  
 Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu  
 130 135 140  
  
 Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr  
 145 150 155 160

Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg  
 165 170 175  
 Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val  
 180 185 190  
 His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu  
 195 200 205  
 Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile  
 210 215 220  
 Leu Tyr Arg Thr Ala Arg Thr Gln Ile Gly Ser Lys Phe Thr Arg Trp  
 225 230 235 240  
 Gly Ser Gln Gly Glu Arg Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu  
 245 250 255  
 Ser Arg Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala  
 260 265 270  
 Val Glu Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr  
 275 280 285  
 Asn Arg Val Ile Phe Leu Glu Asp Asp Asp Val Ala Ala Val Val Asp  
 290 295 300  
 Gly Arg Leu Ser Ile His Arg Ile Lys Arg Thr Ala Gly Asp His Pro  
 305 310 315 320  
 Gly Arg Ala Val Gln Thr Leu Gln Met Glu Leu Gln Gln Ile Met Lys  
 325 330 335  
 Gly Asn Phe Ser Ser Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Glu  
 340 345 350  
 Ser Val Val Asn Thr Met Arg Gly Arg Val Asn Phe Asp Asp Tyr Thr  
 355 360 365  
 Val Asn Leu Gly Gly Leu Lys Asp His Ile Lys Glu Ile Gln Arg Cys  
 370 375 380  
 Arg Arg Leu Ile Leu Ile Ala Cys Gly Thr Ser Tyr His Ala Gly Val  
 385 390 395 400  
 Ala Thr Arg Gln Val Leu Glu Glu Leu Thr Glu Leu Pro Val Met Val  
 405 410 415  
 Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn Thr Pro Val Phe Arg Asp  
 420 425 430  
 Asp Val Cys Phe Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp Thr Leu  
 435 440 445  
 Met Gly Leu Arg Tyr Cys Lys Glu Arg Gly Ala Leu Thr Val Gly Ile  
 450 455 460  
 Thr Asn Thr Val Gly Ser Ser Ile Ser Arg Glu Thr Asp Cys Gly Val  
 465 470 475 480  
 His Ile Asn Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr



485

490

495

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Thr Ser Gln Phe Val Ser Leu Val Met Phe Ala Leu Met Met Cys Asp
      500                      505                      510

Asp Arg Ile Ser Met Gln Glu Arg Arg Lys Glu Ile Met Leu Gly Leu
      515                      520                      525

Lys Arg Leu Pro Asp Leu Ile Lys Glu Val Leu Ser Met Asp Asp Glu
      530                      535                      540

Ile Gln Lys Leu Ala Thr Glu Leu Tyr His Gln Lys Ser Val Leu Ile
545                      550                      555                      560

Met Gly Arg Gly Tyr His Tyr Ala Thr Cys Leu Glu Gly Ala Leu Lys
      565                      570                      575

Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly Ile Leu Ala Gly Glu
      580                      585                      590

Leu Lys His Gly Pro Leu Ala Leu Val Asp Lys Leu Met Pro Val Ile
      595                      600                      605

Met Ile Ile Met Arg Asp His Thr Tyr Ala Lys Cys Gln Asn Ala Leu
      610                      615                      620

Gln Gln Val Val Ala Arg Gln Gly Arg Pro Val Val Ile Cys Asp Lys
625                      630                      635                      640

Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr Ile Lys Val Pro
      645                      650                      655

His Ser Val Asp Cys Leu Gln Gly Ile Leu Ser Val Ile Pro Leu Gln
      660                      665                      670

Leu Leu Ala Phe His Leu Ala Val Leu Arg Gly Tyr Asp Val Asp Phe
      675                      680                      685

Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu
      690                      695

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<210> 7
<211> 2064
<212> DNA
<213> Artificial sequence

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<220>
<223> modified GFAT1 by an internal purification tag

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<220>
<221> CDS
<222> (1)..(2064)
<223>

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<220>
<221> misc_feature
<222> (170)..(170)
<223> t or c

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<400> 7	
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cga gaa atc ctg gag acc cta atc aaa ggc ctt cag aga ctg gag tac Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr 20 25 30	96
aga gga tat gat tct gct ggt gtg gga ttt gat gga ggc aat gat aaa Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys 35 40 45	144
gat tgg gaa gcc aat gcc tgc aaa anc cag ctt att aag aag aaa gga Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly 50 55 60	192
aaa gtt aag gca ctg gat gaa gaa gtt cac aag caa caa gat atg gat Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp 65 70 75 80	240
ttg gat ata gaa ttt gat gta cac ctt gga ata gct cat acc cgt tgg Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp 85 90 95	288
gca aca cat gga gaa ccc agt cct gtc aat agc cac ccc cag cgc tct Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser 100 105 110	336
gat aaa aat aat gaa ttt atc gtt att cac aat gga atc atc acc aac Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn 115 120 125	384
tac aaa gac ttg aaa aag ttt ttg gaa agc aaa ggc tat gac ttc gaa Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu 130 135 140	432
tct gaa aca gac aca gag aca att gcc aag ctc gtt aag tat atg tat Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr 145 150 155 160	480
gac aat cgg gaa agt caa gat acc agc ttt act acc ttg gtg gag aga Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg 165 170 175	528
gtt atc caa caa ttg gaa ggt gct ttt gca ctt gtg ttt aaa agt gtt Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val 180 185 190	576
cat ttt ccc ggg caa gca gtt ggc aca agg cga ggt agc cct ctg ttg His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu 195 200 205	624
att ggt gta cgg agt gaa cat aaa ctt tct act gat cac att cct ata Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile 210 215 220	672
ctc tac aga aca ggc aaa gac aag aaa gga agc tgc aat ctc tct cgt	720

Leu 225	Tyr	Arg	Thr	Gly	Lys 230	Asp	Lys	Lys	Gly	Ser 235	Cys	Asn	Leu	Ser	Arg 240	
gtg	gac	agc	aca	acc	tgc	ctt	ttc	ccg	gtg	gaa	gaa	aaa	gca	gtg	gag	768
Val	Asp	Ser	Thr	Thr	Cys	Leu	Phe	Pro	Val	Glu	Glu	Lys	Ala	Val	Glu	
				245					250					255		
tat	tac	ttt	gct	tct	gat	gca	agt	gct	gtc	ata	gaa	cac	acc	aat	cgc	816
Tyr	Tyr	Phe	Ala	Ser	Asp	Ala	Ser	Ala	Val	Ile	Glu	His	Thr	Asn	Arg	
			260					265					270			
gtc	atc	ttt	ctg	gaa	gat	gat	gat	gtt	gca	gca	gta	gtg	gat	gga	cgt	864
Val	Ile	Phe	Leu	Glu	Asp	Asp	Asp	Val	Ala	Ala	Val	Val	Asp	Gly	Arg	
		275					280					285				
ctt	tct	atc	cat	cga	att	aaa	cga	act	gca	gga	cat	cac	cat	cac	cat	912
Leu	Ser	Ile	His	Arg	Ile	Lys	Arg	Thr	Ala	Gly	His	His	His	His	His	
		290				295					300					
cac	gat	cac	ccc	gga	cga	gct	gtg	caa	aca	ctc	cag	atg	gaa	ctc	cag	960
His	Asp	His	Pro	Gly	Arg	Ala	Val	Gln	Thr	Leu	Gln	Met	Glu	Leu	Gln	
305					310					315					320	
cag	atc	atg	aag	ggc	aac	ttc	agt	tca	ttt	atg	cag	aag	gaa	ata	ttt	1008
Gln	Ile	Met	Lys	Gly	Asn	Phe	Ser	Ser	Phe	Met	Gln	Lys	Glu	Ile	Phe	
				325					330					335		
gag	cag	cca	gag	tct	gtc	gtg	aac	aca	atg	aga	gga	aga	gtc	aac	ttt	1056
Glu	Gln	Pro	Glu	Ser	Val	Val	Asn	Thr	Met	Arg	Gly	Arg	Val	Asn	Phe	
			340					345					350			
gat	gac	tat	act	gtg	aat	ttg	ggg	ggg	ttg	aag	gat	cac	ata	aag	gag	1104
Asp	Asp	Tyr	Thr	Val	Asn	Leu	Gly	Gly	Leu	Lys	Asp	His	Ile	Lys	Glu	
		355					360					365				
atc	cag	aga	tgc	cgg	cgt	ttg	att	ctt	att	gct	tgt	gga	aca	agt	tac	1152
Ile	Gln	Arg	Cys	Arg	Arg	Leu	Ile	Leu	Ile	Ala	Cys	Gly	Thr	Ser	Tyr	
		370				375					380					
cat	gct	ggg	gta	gca	aca	cgt	caa	gtt	ctt	gag	gag	ctg	act	gag	ttg	1200
His	Ala	Gly	Val	Ala	Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr	Glu	Leu	
385					390					395					400	
cct	gtg	atg	gtg	gaa	cta	gca	agt	gac	ttc	ctg	gac	aga	aac	aca	cca	1248
Pro	Val	Met	Val	Glu	Leu	Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn	Thr	Pro	
				405					410					415		
gtc	ttt	cga	gat	gat	gtt	tgc	ttt	ttc	ctt	agt	caa	tca	ggg	gag	aca	1296
Val	Phe	Arg	Asp	Asp	Val	Cys	Phe	Phe	Leu	Ser	Gln	Ser	Gly	Glu	Thr	
			420					425					430			
gca	gat	act	ttg	atg	ggg	ctt	cgt	tac	tgt	aag	gag	aga	gga	gct	tta	1344
Ala	Asp	Thr	Leu	Met	Gly	Leu	Arg	Tyr	Cys	Lys	Glu	Arg	Gly	Ala	Leu	
		435				440						445				
act	gtg	ggg	atc	aca	aac	aca	gtt	ggc	agt	tcc	ata	tca	cgg	gag	aca	1392
Thr	Val	Gly	Ile	Thr	Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	Glu	Thr	
		450				455					460					
gat	tgt	gga	gtt	cat	att	aat	gct	ggg	cct	gag	att	ggg	gtg	gcc	agt	1440
Asp	Cys	Gly	Val	His	Ile	Asn	Ala	Gly	Pro	Glu	Ile	Gly	Val	Ala	Ser	

465	470	475	480	
aca aag gct tat acc agc cag ttt gta tcc ctt gtg atg ttt gcc ctt				1488
Thr Lys Ala Tyr	Thr Ser Gln Phe	Val Ser Leu Val	Met Phe Ala Leu	
	485	490	495	
atg atg tgt gat gat cgg atc tcc atg caa gaa aga cgc aaa gag atc				1536
Met Met Cys Asp Asp Arg Ile Ser Met Gln Glu Arg Arg Lys Glu Ile				
	500	505	510	
atg ctt gga ttg aaa cgg ctg cct gat ttg att aag gaa gta ctg agc				1584
Met Leu Gly Leu Lys Arg Leu Pro Asp Leu Ile Lys Glu Val Leu Ser				
	515	520	525	
atg gat gac gaa att cag aaa cta gca aca gaa ctt tat cat cag aag				1632
Met Asp Asp Glu Ile Gln Lys Leu Ala Thr Glu Leu Tyr His Gln Lys				
	530	535	540	
tca gtt ctg ata atg gga cga ggc tat cat tat gct act tgt ctt gaa				1680
Ser Val Leu Ile Met Gly Arg Gly Tyr His Tyr Ala Thr Cys Leu Glu				
	545	550	555	560
ggg gca ctg aaa atc aaa gaa att act tat atg cac tct gaa ggc atc				1728
Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly Ile				
	565	570	575	
ctt gct ggt gaa ttg aaa cat ggc cct ctg gct ttg gtg gat aaa ttg				1776
Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Val Asp Lys Leu				
	580	585	590	
atg cct gtg atc atg atc atc atg aga gat cac act tat gcc aag tgt				1824
Met Pro Val Ile Met Ile Ile Met Arg Asp His Thr Tyr Ala Lys Cys				
	595	600	605	
cag aat gct ctt cag caa gtg gtt gct cgg cag ggg cgg cct gtg gta				1872
Gln Asn Ala Leu Gln Gln Val Val Ala Arg Gln Gly Arg Pro Val Val				
	610	615	620	
att tgt gat aag gag gat act gag acc att aag aac aca aaa aga acg				1920
Ile Cys Asp Lys Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr				
	625	630	635	640
atc aag gtg ccc cac tca gtg gac tgc ttg cag ggc att ctc agc gtg				1968
Ile Lys Val Pro His Ser Val Asp Cys Leu Gln Gly Ile Leu Ser Val				
	645	650	655	
atc cct tta cag ttg ctg gct ttc cac ctt gct gtg ctg aga ggc tat				2016
Ile Pro Leu Gln Leu Leu Ala Phe His Leu Ala Val Leu Arg Gly Tyr				
	660	665	670	
gat gtt gat ttc cca cgg aat ctt gcc aaa tct gtg act gta gag tga				2064
Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu				
	675	680	685	

<210> 8  
 <211> 687  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> (57)..(57)  
 <223> 'Xaa' in position 57 represents Thr or Ile

<220>  
 <223> modified GFAT1 by an internal purification tag

<400> 8  
 Met Cys Gly Ile Phe Ala Tyr Leu Asn Tyr His Val Pro Arg Thr Arg  
 1 5 10 15  
 Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr  
 20 25 30  
 Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys  
 35 40 45  
 Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly  
 50 55 60  
 Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp  
 65 70 75 80  
 Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp  
 85 90 95  
 Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser  
 100 105 110  
 Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn  
 115 120 125  
 Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu  
 130 135 140  
 Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr  
 145 150 155 160  
 Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg  
 165 170 175  
 Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val  
 180 185 190  
 His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu  
 195 200 205  
 Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile  
 210 215 220  
 Leu Tyr Arg Thr Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu Ser Arg  
 225 230 235 240  
 Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala Val Glu  
 245 250 255  
 Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr Asn Arg  
 260 265 270  
 Val Ile Phe Leu Glu Asp Asp Asp Val Ala Ala Val Val Asp Gly Arg

275

280

285

Leu	Ser	Ile	His	Arg	Ile	Lys	Arg	Thr	Ala	Gly	His	His	His	His	His
290						295					300				
His	Asp	His	Pro	Gly	Arg	Ala	Val	Gln	Thr	Leu	Gln	Met	Glu	Leu	Gln
305					310					315					320
Gln	Ile	Met	Lys	Gly	Asn	Phe	Ser	Ser	Phe	Met	Gln	Lys	Glu	Ile	Phe
				325					330					335	
Glu	Gln	Pro	Glu	Ser	Val	Val	Asn	Thr	Met	Arg	Gly	Arg	Val	Asn	Phe
			340					345					350		
Asp	Asp	Tyr	Thr	Val	Asn	Leu	Gly	Gly	Leu	Lys	Asp	His	Ile	Lys	Glu
		355					360					365			
Ile	Gln	Arg	Cys	Arg	Arg	Leu	Ile	Leu	Ile	Ala	Cys	Gly	Thr	Ser	Tyr
370						375					380				
His	Ala	Gly	Val	Ala	Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr	Glu	Leu
385					390					395					400
Pro	Val	Met	Val	Glu	Leu	Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn	Thr	Pro
				405					410					415	
Val	Phe	Arg	Asp	Asp	Val	Cys	Phe	Phe	Leu	Ser	Gln	Ser	Gly	Glu	Thr
			420					425					430		
Ala	Asp	Thr	Leu	Met	Gly	Leu	Arg	Tyr	Cys	Lys	Glu	Arg	Gly	Ala	Leu
		435					440					445			
Thr	Val	Gly	Ile	Thr	Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	Glu	Thr
450						455					460				
Asp	Cys	Gly	Val	His	Ile	Asn	Ala	Gly	Pro	Glu	Ile	Gly	Val	Ala	Ser
465					470					475					480
Thr	Lys	Ala	Tyr	Thr	Ser	Gln	Phe	Val	Ser	Leu	Val	Met	Phe	Ala	Leu
				485					490					495	
Met	Met	Cys	Asp	Asp	Arg	Ile	Ser	Met	Gln	Glu	Arg	Arg	Lys	Glu	Ile
			500					505					510		
Met	Leu	Gly	Leu	Lys	Arg	Leu	Pro	Asp	Leu	Ile	Lys	Glu	Val	Leu	Ser
		515					520					525			
Met	Asp	Asp	Glu	Ile	Gln	Lys	Leu	Ala	Thr	Glu	Leu	Tyr	His	Gln	Lys
530						535					540				
Ser	Val	Leu	Ile	Met	Gly	Arg	Gly	Tyr	His	Tyr	Ala	Thr	Cys	Leu	Glu
545					550					555					560
Gly	Ala	Leu	Lys	Ile	Lys	Glu	Ile	Thr	Tyr	Met	His	Ser	Glu	Gly	Ile
				565					570					575	
Leu	Ala	Gly	Glu	Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Val	Asp	Lys	Leu
			580					585					590		
Met	Pro	Val	Ile	Met	Ile	Ile	Met	Arg	Asp	His	Thr	Tyr	Ala	Lys	Cys

595 600 605

Gln Asn Ala Leu Gln Gln Val Val Ala Arg Gln Gly Arg Pro Val Val  
610 615 620

Ile Cys Asp Lys Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys Arg Thr  
625 630 635 640

Ile Lys Val Pro His Ser Val Asp Cys Leu Gln Gly Ile Leu Ser Val  
645 650 655

Ile Pro Leu Gln Leu Leu Ala Phe His Leu Ala Val Leu Arg Gly Tyr  
660 665 670

Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu  
675 680 685

<210> 9  
<211> 2067  
<212> DNA  
<213> Artificial sequence

<220>  
<223> modified GFAT2 by an internal purification tag

<220>  
<221> CDS  
<222> (1)..(2067)  
<223>

<400> 9

atg tgc gga atc ttt gcc tac atg aac tac aga gtc ccc cgg acg agg	48
Met Cys Gly Ile Phe Ala Tyr Met Asn Tyr Arg Val Pro Arg Thr Arg	
1 5 10 15	
aag gag atc ttc gaa acc ctc atc aag ggc ctg cag cgg ctg gag tac	96
Lys Glu Ile Phe Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr	
20 25 30	
aga ggc tac gac tcg gca ggt gtg gcg atc gat ggg aat aat cac gaa	144
Arg Gly Tyr Asp Ser Ala Gly Val Ala Ile Asp Gly Asn Asn His Glu	
35 40 45	
gtc aaa gaa aga cac att cag ctg gtc aag aaa agg ggg aaa gtc aag	192
Val Lys Glu Arg His Ile Gln Leu Val Lys Lys Arg Gly Lys Val Lys	
50 55 60	
gct ctc gat gaa gaa ctt tac aaa caa gac agc atg gac tta aaa gtg	240
Ala Leu Asp Glu Glu Leu Tyr Lys Gln Asp Ser Met Asp Leu Lys Val	
65 70 75 80	
gag ttt gag aca cac ttc ggc att gcc cac acg cgc tgg gcc acc cac	288
Glu Phe Glu Thr His Phe Gly Ile Ala His Thr Arg Trp Ala Thr His	
85 90 95	
ggg gtc ccc agt gct gtc aac agc cac cct cag cgc tca gac aaa ggc	336
Gly Val Pro Ser Ala Val Asn Ser His Pro Gln Arg Ser Asp Lys Gly	
100 105 110	

aac gaa ttt gtt gtc atc cac aat ggg atc atc aca aat tac aaa gat Asn Glu Phe Val Val Ile His Asn Gly Ile Ile Thr Asn Tyr Lys Asp 115 120 125	384
ctg agg aaa ttt ctg gaa agc aaa ggc tac gag ttt gag tca gaa aca Leu Arg Lys Phe Leu Glu Ser Lys Gly Tyr Glu Phe Glu Ser Glu Thr 130 135 140	432
gat aca gag acc atc gcc aag ctg att aaa tat gtg ttc gac aac aga Asp Thr Glu Thr Ile Ala Lys Leu Ile Lys Tyr Val Phe Asp Asn Arg 145 150 155 160	480
gaa act gag gac att acg ttt tca acg ttg gtc gag aga gtc att cag Glu Thr Glu Asp Ile Thr Phe Ser Thr Leu Val Glu Arg Val Ile Gln 165 170 175	528
cag ttg gaa ggt gca ttc gcg ctg gtt ttc aag agt gtc cac tac cca Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val His Tyr Pro 180 185 190	576
gga gaa gcc gtt gcc aca cgg aga ggc agc ccc ctg ctc atc gga gtc Gly Glu Ala Val Ala Thr Arg Arg Gly Ser Pro Leu Leu Ile Gly Val 195 200 205	624
cgg agc aaa tac aag ctc tcc aca gaa cag atc cct atc tta tac agg Arg Ser Lys Tyr Lys Leu Ser Thr Glu Gln Ile Pro Ile Leu Tyr Arg 210 215 220	672
acg tgc act ctg gag aat gtg aag aat atc tgt aag aca cgg atg aag Thr Cys Thr Leu Glu Asn Val Lys Asn Ile Cys Lys Thr Arg Met Lys 225 230 235 240	720
agg ctg gac agc tcc gcc tgc ctg cat gct gtg ggc gac aag gcc gtg Arg Leu Asp Ser Ser Ala Cys Leu His Ala Val Gly Asp Lys Ala Val 245 250 255	768
gaa ttc ttc ttt gct tct gat gca agc gct atc ata gag cac acc aac Glu Phe Phe Phe Ala Ser Asp Ala Ser Ala Ile Ile Glu His Thr Asn 260 265 270	816
cgg gtc atc ttc ctg gag gac gat gac atc gcc gca gtg gct gat ggg Arg Val Ile Phe Leu Glu Asp Asp Asp Ile Ala Ala Val Ala Asp Gly 275 280 285	864
aaa ctc tcc att cac cgg gtc aag cgc tcg gcc agt cat cac cat cac Lys Leu Ser Ile His Arg Val Lys Arg Ser Ala Ser His His His His 290 295 300	912
cat cac gat gac cca tct cga gcc atc cag acc ttg cag atg gaa ctg His His Asp Asp Pro Ser Arg Ala Ile Gln Thr Leu Gln Met Glu Leu 305 310 315 320	960
cag caa atc atg aaa ggt aac ttc agt gcg ttt atg cag aag gag atc Gln Gln Ile Met Lys Gly Asn Phe Ser Ala Phe Met Gln Lys Glu Ile 325 330 335	1008
ttc gaa cag cca gaa tca gtt ttc aat act atg aga ggt cgg gtg aat Phe Glu Gln Pro Glu Ser Val Phe Asn Thr Met Arg Gly Arg Val Asn 340 345 350	1056
ttt gaa acc aac aca gtg ctc ctg ggt ggc ttg aag gac cac ttg aag	1104



Phe	Glu	Thr	Asn	Thr	Val	Leu	Leu	Gly	Gly	Leu	Lys	Asp	His	Leu	Lys	
		355					360					365				
gag	att	cga	cga	tgc	cga	cgg	ctc	atc	gtg	att	ggc	tgt	gga	acc	agc	1152
Glu	Ile	Arg	Arg	Cys	Arg	Arg	Leu	Ile	Val	Ile	Gly	Cys	Gly	Thr	Ser	
	370					375					380					
tac	cac	gct	gcc	gtg	gct	acg	cgg	caa	gtt	ttg	gag	gaa	ctg	act	gag	1200
Tyr	His	Ala	Ala	Val	Ala	Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr	Glu	
385					390					395					400	
ctt	cct	gtg	atg	gtt	gaa	ctt	gct	agt	gat	ttt	ctg	gac	agg	aac	aca	1248
Leu	Pro	Val	Met	Val	Glu	Leu	Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn	Thr	
				405					410					415		
cct	gtg	ttc	agg	gat	gac	gtt	tgc	ttt	ttc	atc	agc	cag	tca	ggc	gag	1296
Pro	Val	Phe	Arg	Asp	Asp	Val	Cys	Phe	Phe	Ile	Ser	Gln	Ser	Gly	Glu	
			420					425					430			
acc	gcg	gac	acc	ctc	ctg	gcg	ctg	cgc	tac	tgt	aag	gac	cgc	ggc	gct	1344
Thr	Ala	Asp	Thr	Leu	Leu	Ala	Leu	Arg	Tyr	Cys	Lys	Asp	Arg	Gly	Ala	
		435					440					445				
ctc	acc	gtg	ggc	gtc	acc	aac	acc	gtg	ggc	agc	tcc	atc	tct	cgc	gag	1392
Leu	Thr	Val	Gly	Val	Thr	Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	Glu	
	450					455					460					
acc	gac	tgc	ggc	gtc	cac	atc	aac	gca	ggg	ccg	gag	gtc	ggc	gtg	gcc	1440
Thr	Asp	Cys	Gly	Val	His	Ile	Asn	Ala	Gly	Pro	Glu	Val	Gly	Val	Ala	
465					470					475					480	
agc	acc	aag	gct	tat	acc	agt	cag	ttc	atc	tct	ctg	gtg	atg	ttt	ggc	1488
Ser	Thr	Lys	Ala	Tyr	Thr	Ser	Gln	Phe	Ile	Ser	Leu	Val	Met	Phe	Gly	
			485						490					495		
ttg	atg	atg	tct	gaa	gac	cga	att	tca	cta	caa	aac	agg	agg	caa	gag	1536
Leu	Met	Met	Ser	Glu	Asp	Arg	Ile	Ser	Leu	Gln	Asn	Arg	Arg	Gln	Glu	
			500					505					510			
atc	atc	cgt	ggc	ttg	aga	tct	tta	cct	gag	ctg	atc	aag	gaa	gtg	ctg	1584
Ile	Ile	Arg	Gly	Leu	Arg	Ser	Leu	Pro	Glu	Leu	Ile	Lys	Glu	Val	Leu	
		515					520					525				
tct	ctg	gag	gag	aag	atc	cac	gac	ttg	gcc	ctg	gag	ctc	tac	acg	cag	1632
Ser	Leu	Glu	Glu	Lys	Ile	His	Asp	Leu	Ala	Leu	Glu	Leu	Tyr	Thr	Gln	
	530					535					540					
aga	tcg	ctg	ctg	gtg	atg	ggg	cgg	ggc	tac	aac	tat	gcc	acc	tgc	ctg	1680
Arg	Ser	Leu	Leu	Val	Met	Gly	Arg	Gly	Tyr	Asn	Tyr	Ala	Thr	Cys	Leu	
545					550					555					560	
gaa	gga	gcc	ctg	aaa	att	aaa	gag	ata	acc	tac	atg	cac	tca	gaa	ggc	1728
Glu	Gly	Ala	Leu	Lys	Ile	Lys	Glu	Ile	Thr	Tyr	Met	His	Ser	Glu	Gly	
				565					570					575		
atc	ctg	gct	ggg	gag	ctg	aag	cac	ggg	ccc	ctg	gca	ctg	att	gac	aag	1776
Ile	Leu	Ala	Gly	Glu	Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Ile	Asp	Lys	
			580					585					590			
cag	atg	ccc	gtc	atc	atg	gtc	att	atg	aag	gat	cct	tgc	ttc	gcc	aaa	1824
Gln	Met	Pro	Val	Ile	Met	Val	Ile	Met	Lys	Asp	Pro	Cys	Phe	Ala	Lys	

595	600	605	
tgc cag aac gcc ctg cag caa gtc acg gcc cgc cag ggt cgc ccc att			1872
Cys Gln Asn Ala Leu Gln Gln Val Thr Ala Arg Gln Gly Arg Pro Ile			
610	615	620	
ata ctg tgc tcc aag gac gat act gaa agt tcc aag ttt gcg tat aag			1920
Ile Leu Cys Ser Lys Asp Asp Thr Glu Ser Ser Lys Phe Ala Tyr Lys			
625	630	635	640
aca atc gag ctg ccc cac act gtg gac tgc ctc cag ggc atc ctg agc			1968
Thr Ile Glu Leu Pro His Thr Val Asp Cys Leu Gln Gly Ile Leu Ser			
645	650	655	
gtg att ccg ctg cag ctg ctg tcc ttc cac ctg gct gtt ctc cga gga			2016
Val Ile Pro Leu Gln Leu Leu Ser Phe His Leu Ala Val Leu Arg Gly			
660	665	670	
tat gac gtt gac ttc ccc aga aat ctg gcc aag tct gta act gtg gaa			2064
Tyr Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu			
675	680	685	
tga			2067

<210> 10  
 <211> 688  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> modified GFAT2 by an internal purification tag

<400> 10  
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 Lys Glu Ile Phe Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr  
 20 25 30  
 Arg Gly Tyr Asp Ser Ala Gly Val Ala Ile Asp Gly Asn Asn His Glu  
 35 40 45  
 Val Lys Glu Arg His Ile Gln Leu Val Lys Lys Arg Gly Lys Val Lys  
 50 55 60  
 Ala Leu Asp Glu Glu Leu Tyr Lys Gln Asp Ser Met Asp Leu Lys Val  
 65 70 75 80  
 Glu Phe Glu Thr His Phe Gly Ile Ala His Thr Arg Trp Ala Thr His  
 85 90 95  
 Gly Val Pro Ser Ala Val Asn Ser His Pro Gln Arg Ser Asp Lys Gly  
 100 105 110  
 Asn Glu Phe Val Val Ile His Asn Gly Ile Ile Thr Asn Tyr Lys Asp  
 115 120 125  
 Leu Arg Lys Phe Leu Glu Ser Lys Gly Tyr Glu Phe Glu Ser Glu Thr  
 130 135 140

Asp	Thr	Glu	Thr	Ile	Ala	Lys	Leu	Ile	Lys	Tyr	Val	Phe	Asp	Asn	Arg	
145					150					155					160	
Glu	Thr	Glu	Asp	Ile	Thr	Phe	Ser	Thr	Leu	Val	Glu	Arg	Val	Ile	Gln	
				165					170					175		
Gln	Leu	Glu	Gly	Ala	Phe	Ala	Leu	Val	Phe	Lys	Ser	Val	His	Tyr	Pro	
			180					185					190			
Gly	Glu	Ala	Val	Ala	Thr	Arg	Arg	Gly	Ser	Pro	Leu	Leu	Ile	Gly	Val	
		195					200					205				
Arg	Ser	Lys	Tyr	Lys	Leu	Ser	Thr	Glu	Gln	Ile	Pro	Ile	Leu	Tyr	Arg	
	210					215					220					
Thr	Cys	Thr	Leu	Glu	Asn	Val	Lys	Asn	Ile	Cys	Lys	Thr	Arg	Met	Lys	
225					230					235					240	
Arg	Leu	Asp	Ser	Ser	Ala	Cys	Leu	His	Ala	Val	Gly	Asp	Lys	Ala	Val	
				245					250					255		
Glu	Phe	Phe	Phe	Ala	Ser	Asp	Ala	Ser	Ala	Ile	Ile	Glu	His	Thr	Asn	
			260					265					270			
Arg	Val	Ile	Phe	Leu	Glu	Asp	Asp	Asp	Ile	Ala	Ala	Val	Ala	Asp	Gly	
		275					280					285				
Lys	Leu	Ser	Ile	His	Arg	Val	Lys	Arg	Ser	Ala	Ser	His	His	His	His	
	290					295					300					
His	His	Asp	Asp	Pro	Ser	Arg	Ala	Ile	Gln	Thr	Leu	Gln	Met	Glu	Leu	
305					310					315					320	
Gln	Gln	Ile	Met	Lys	Gly	Asn	Phe	Ser	Ala	Phe	Met	Gln	Lys	Glu	Ile	
			325						330					335		
Phe	Glu	Gln	Pro	Glu	Ser	Val	Phe	Asn	Thr	Met	Arg	Gly	Arg	Val	Asn	
			340					345					350			
Phe	Glu	Thr	Asn	Thr	Val	Leu	Leu	Gly	Gly	Leu	Lys	Asp	His	Leu	Lys	
		355					360					365				
Glu	Ile	Arg	Arg	Cys	Arg	Arg	Leu	Ile	Val	Ile	Gly	Cys	Gly	Thr	Ser	
	370					375					380					
Tyr	His	Ala	Ala	Val	Ala	Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr	Glu	
385					390					395					400	
Leu	Pro	Val	Met	Val	Glu	Leu	Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn	Thr	
				405					410					415		
Pro	Val	Phe	Arg	Asp	Asp	Val	Cys	Phe	Phe	Ile	Ser	Gln	Ser	Gly	Glu	
			420					425					430			
Thr	Ala	Asp	Thr	Leu	Leu	Ala	Leu	Arg	Tyr	Cys	Lys	Asp	Arg	Gly	Ala	
		435					440					445				
Leu	Thr	Val	Gly	Val	Thr	Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	Glu	
	450					455					460					

Thr Asp Cys Gly Val His Ile Asn Ala Gly Pro Glu Val Gly Val Ala  
 465 470 475 480  
 Ser Thr Lys Ala Tyr Thr Ser Gln Phe Ile Ser Leu Val Met Phe Gly  
 485 490 495  
 Leu Met Met Ser Glu Asp Arg Ile Ser Leu Gln Asn Arg Arg Gln Glu  
 500 505 510  
 Ile Ile Arg Gly Leu Arg Ser Leu Pro Glu Leu Ile Lys Glu Val Leu  
 515 520 525  
 Ser Leu Glu Glu Lys Ile His Asp Leu Ala Leu Glu Leu Tyr Thr Gln  
 530 535 540  
 Arg Ser Leu Leu Val Met Gly Arg Gly Tyr Asn Tyr Ala Thr Cys Leu  
 545 550 555 560  
 Glu Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu Gly  
 565 570 575  
 Ile Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp Lys  
 580 585 590  
 Gln Met Pro Val Ile Met Val Ile Met Lys Asp Pro Cys Phe Ala Lys  
 595 600 605  
 Cys Gln Asn Ala Leu Gln Gln Val Thr Ala Arg Gln Gly Arg Pro Ile  
 610 615 620  
 Ile Leu Cys Ser Lys Asp Asp Thr Glu Ser Ser Lys Phe Ala Tyr Lys  
 625 630 635 640  
 Thr Ile Glu Leu Pro His Thr Val Asp Cys Leu Gln Gly Ile Leu Ser  
 645 650 655  
 Val Ile Pro Leu Gln Leu Leu Ser Phe His Leu Ala Val Leu Arg Gly  
 660 665 670  
 Tyr Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu  
 675 680 685

<210> 11  
 <211> 2118  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> modified GFAT1Alt by an internal purification tag

<220>  
 <221> CDS  
 <222> (1)..(2118)  
 <223>

<220>  
 <221> misc\_feature  
 <222> (170)..(170)  
 <223> t or c

<400> 11

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Met Cys Gly Ile Phe Ala Tyr Leu Asn Tyr His Val Pro Arg Thr Arg	
1 5 10 15	
cga gaa atc ctg gag acc cta atc aaa ggc ctt cag aga ctg gag tac	96
Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr	
20 25 30	
aga gga tat gat tct gct ggt gtg gga ttt gat gga ggc aat gat aaa	144
Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys	
35 40 45	
gat tgg gaa gcc aat gcc tgc aaa anc cag ctt att aag aag aaa gga	192
Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly	
50 55 60	
aaa gtt aag gca ctg gat gaa gaa gtt cac aag caa caa gat atg gat	240
Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp	
65 70 75 80	
ttg gat ata gaa ttt gat gta cac ctt gga ata gct cat acc cgt tgg	288
Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp	
85 90 95	
gca aca cat gga gaa ccc agt cct gtc aat agc cac ccc cag cgc tct	336
Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser	
100 105 110	
gat aaa aat aat gaa ttt atc gtt att cac aat gga atc atc acc aac	384
Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn	
115 120 125	
tac aaa gac ttg aaa aag ttt ttg gaa agc aaa ggc tat gac ttc gaa	432
Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu	
130 135 140	
tct gaa aca gac aca gag aca att gcc aag ctc gtt aag tat atg tat	480
Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr	
145 150 155 160	
gac aat cgg gaa agt caa gat acc agc ttt act acc ttg gtg gag aga	528
Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg	
165 170 175	
gtt atc caa caa ttg gaa ggt gct ttt gca ctt gtg ttt aaa agt gtt	576
Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val	
180 185 190	
cat ttt ccc ggg caa gca gtt ggc aca agg cga ggt agc cct ctg ttg	624
His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu	
195 200 205	
att ggt gta cgg agt gaa cat aaa ctt tct act gat cac att cct ata	672
Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile	
210 215 220	
ctc tac aga aca gct agg act cag att gga tca aaa ttc aca cgg tgg	720

Leu 225	Tyr	Arg	Thr	Ala	Arg 230	Thr	Gln	Ile	Gly	Ser 235	Lys	Phe	Thr	Arg	Trp 240	
gga	tca	cag	gga	gaa	aga	ggc	aaa	gac	aag	aaa	gga	agc	tgc	aat	ctc	768
Gly	Ser	Gln	Gly	Glu	Arg	Gly	Lys	Asp	Lys	Lys	Gly	Ser	Cys	Asn	Leu	
				245					250					255		
tct	cgt	gtg	gac	agc	aca	acc	tgc	ctt	ttc	ccg	gtg	gaa	gaa	aaa	gca	816
Ser	Arg	Val	Asp	Ser	Thr	Thr	Cys	Leu	Phe	Pro	Val	Glu	Glu	Lys	Ala	
			260					265					270			
gtg	gag	tat	tac	ttt	gct	tct	gat	gca	agt	gct	gtc	ata	gaa	cac	acc	864
Val	Glu	Tyr	Tyr	Phe	Ala	Ser	Asp	Ala	Ser	Ala	Val	Ile	Glu	His	Thr	
		275					280					285				
aat	cgc	gtc	atc	ttt	ctg	gaa	gat	gat	gat	gtt	gca	gca	gta	gtg	gat	912
Asn	Arg	Val	Ile	Phe	Leu	Glu	Asp	Asp	Asp	Val	Ala	Ala	Val	Val	Asp	
	290					295					300					
gga	cgt	ctt	tct	atc	cat	cga	att	aaa	cga	act	gca	gga	cat	cac	cat	960
Gly	Arg	Leu	Ser	Ile	His	Arg	Ile	Lys	Arg	Thr	Ala	Gly	His	His	His	
305					310					315					320	
cac	cat	cac	gat	cac	ccc	gga	cga	gct	gtg	caa	aca	ctc	cag	atg	gaa	1008
His	His	His	Asp	His	Pro	Gly	Arg	Ala	Val	Gln	Thr	Leu	Gln	Met	Glu	
				325					330					335		
ctc	cag	cag	atc	atg	aag	ggc	aac	ttc	agt	tca	ttt	atg	cag	aag	gaa	1056
Leu	Gln	Gln	Ile	Met	Lys	Gly	Asn	Phe	Ser	Ser	Phe	Met	Gln	Lys	Glu	
			340					345					350			
ata	ttt	gag	cag	cca	gag	tct	gtc	gtg	aac	aca	atg	aga	gga	aga	gtc	1104
Ile	Phe	Glu	Gln	Pro	Glu	Ser	Val	Val	Asn	Thr	Met	Arg	Gly	Arg	Val	
		355					360					365				
aac	ttt	gat	gac	tat	act	gtg	aat	ttg	ggt	ggt	ttg	aag	gat	cac	ata	1152
Asn	Phe	Asp	Asp	Tyr	Thr	Val	Asn	Leu	Gly	Gly	Leu	Lys	Asp	His	Ile	
	370					375					380					
aag	gag	atc	cag	aga	tgc	cgg	cgt	ttg	att	ctt	att	gct	tgt	gga	aca	1200
Lys	Glu	Ile	Gln	Arg	Cys	Arg	Arg	Leu	Ile	Leu	Ile	Ala	Cys	Gly	Thr	
385					390					395					400	
agt	tac	cat	gct	ggt	gta	gca	aca	cgt	caa	ggt	ctt	gag	gag	ctg	act	1248
Ser	Tyr	His	Ala	Gly	Val	Ala	Thr	Arg	Gln	Val	Leu	Glu	Glu	Leu	Thr	
			405					410						415		
gag	ttg	cct	gtg	atg	gtg	gaa	cta	gca	agt	gac	ttc	ctg	gac	aga	aac	1296
Glu	Leu	Pro	Val	Met	Val	Glu	Leu	Ala	Ser	Asp	Phe	Leu	Asp	Arg	Asn	
			420					425					430			
aca	cca	gtc	ttt	cga	gat	gat	ggt	tgc	ttt	ttc	ctt	agt	caa	tca	ggt	1344
Thr	Pro	Val	Phe	Arg	Asp	Asp	Val	Cys	Phe	Phe	Leu	Ser	Gln	Ser	Gly	
		435					440					445				
gag	aca	gca	gat	act	ttg	atg	ggt	ctt	cgt	tac	tgt	aag	gag	aga	gga	1392
Glu	Thr	Ala	Asp	Thr	Leu	Met	Gly	Leu	Arg	Tyr	Cys	Lys	Glu	Arg	Gly	
	450					455					460					
gct	tta	act	gtg	ggg	atc	aca	aac	aca	ggt	ggc	agt	tcc	ata	tca	cgg	1440
Ala	Leu	Thr	Val	Gly	Ile	Thr	Asn	Thr	Val	Gly	Ser	Ser	Ile	Ser	Arg	

465	470	475	480	
gag aca gat tgt gga gtt cat att aat gct ggt cct gag att ggt gtg Glu Thr Asp Cys Gly Val His Ile Asn Ala Gly Pro Glu Ile Gly Val 485 490 495				1488
gcc agt aca aag gct tat acc agc cag ttt gta tcc ctt gtg atg ttt Ala Ser Thr Lys Ala Tyr Thr Ser Gln Phe Val Ser Leu Val Met Phe 500 505 510				1536
gcc ctt atg atg tgt gat gat cgg atc tcc atg caa gaa aga cgc aaa Ala Leu Met Met Cys Asp Asp Arg Ile Ser Met Gln Glu Arg Arg Lys 515 520 525				1584
gag atc atg ctt gga ttg aaa cgg ctg cct gat ttg att aag gaa gta Glu Ile Met Leu Gly Leu Lys Arg Leu Pro Asp Leu Ile Lys Glu Val 530 535 540				1632
ctg agc atg gat gac gaa att cag aaa cta gca aca gaa ctt tat cat Leu Ser Met Asp Asp Glu Ile Gln Lys Leu Ala Thr Glu Leu Tyr His 545 550 555 560				1680
cag aag tca gtt ctg ata atg gga cga ggc tat cat tat gct act tgt Gln Lys Ser Val Leu Ile Met Gly Arg Gly Tyr His Tyr Ala Thr Cys 565 570 575				1728
ctt gaa ggg gca ctg aaa atc aaa gaa att act tat atg cac tct gaa Leu Glu Gly Ala Leu Lys Ile Lys Glu Ile Thr Tyr Met His Ser Glu 580 585 590				1776
ggc atc ctt gct ggt gaa ttg aaa cat ggc cct ctg gct ttg gtg gat Gly Ile Leu Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Val Asp 595 600 605				1824
aaa ttg atg cct gtg atc atg atc atc atg aga gat cac act tat gcc Lys Leu Met Pro Val Ile Met Ile Ile Met Arg Asp His Thr Tyr Ala 610 615 620				1872
aag tgt cag aat gct ctt cag caa gtg gtt gct cgg cag ggg cgg cct Lys Cys Gln Asn Ala Leu Gln Gln Val Val Ala Arg Gln Gly Arg Pro 625 630 635 640				1920
gtg gta att tgt gat aag gag gat act gag acc att aag aac aca aaa Val Val Ile Cys Asp Lys Glu Asp Thr Glu Thr Ile Lys Asn Thr Lys 645 650 655				1968
aga acg atc aag gtg ccc cac tca gtg gac tgc ttg cag ggc att ctc Arg Thr Ile Lys Val Pro His Ser Val Asp Cys Leu Gln Gly Ile Leu 660 665 670				2016
agc gtg atc cct tta cag ttg ctg gct ttc cac ctt gct gtg ctg aga Ser Val Ile Pro Leu Gln Leu Leu Ala Phe His Leu Ala Val Leu Arg 675 680 685				2064
ggc tat gat gtt gat ttc cca cgg aat ctt gcc aaa tct gtg act gta Gly Tyr Asp Val Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val 690 695 700				2112
gag tga Glu				2118

705

<210> 12  
 <211> 705  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> (57)..(57)  
 <223> 'Xaa' in position 57 represents Thr or Ile

<220>  
 <223> modified GFAT1Alt by an internal purification tag

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 Met Cys Gly Ile Phe Ala Tyr Leu Asn Tyr His Val Pro Arg Thr Arg  
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 Arg Glu Ile Leu Glu Thr Leu Ile Lys Gly Leu Gln Arg Leu Glu Tyr  
 20 25 30  
 Arg Gly Tyr Asp Ser Ala Gly Val Gly Phe Asp Gly Gly Asn Asp Lys  
 35 40 45  
 Asp Trp Glu Ala Asn Ala Cys Lys Xaa Gln Leu Ile Lys Lys Lys Gly  
 50 55 60  
 Lys Val Lys Ala Leu Asp Glu Glu Val His Lys Gln Gln Asp Met Asp  
 65 70 75 80  
 Leu Asp Ile Glu Phe Asp Val His Leu Gly Ile Ala His Thr Arg Trp  
 85 90 95  
 Ala Thr His Gly Glu Pro Ser Pro Val Asn Ser His Pro Gln Arg Ser  
 100 105 110  
 Asp Lys Asn Asn Glu Phe Ile Val Ile His Asn Gly Ile Ile Thr Asn  
 115 120 125  
 Tyr Lys Asp Leu Lys Lys Phe Leu Glu Ser Lys Gly Tyr Asp Phe Glu  
 130 135 140  
 Ser Glu Thr Asp Thr Glu Thr Ile Ala Lys Leu Val Lys Tyr Met Tyr  
 145 150 155 160  
 Asp Asn Arg Glu Ser Gln Asp Thr Ser Phe Thr Thr Leu Val Glu Arg  
 165 170 175  
 Val Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Val Phe Lys Ser Val  
 180 185 190  
 His Phe Pro Gly Gln Ala Val Gly Thr Arg Arg Gly Ser Pro Leu Leu  
 195 200 205  
 Ile Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile  
 210 215 220  
 Leu Tyr Arg Thr Ala Arg Thr Gln Ile Gly Ser Lys Phe Thr Arg Trp  
 225 230 235 240



Gly Ser Gln Gly Glu Arg Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu  
 245 250 255  
 Ser Arg Val Asp Ser Thr Thr Cys Leu Phe Pro Val Glu Glu Lys Ala  
 260 265 270  
 Val Glu Tyr Tyr Phe Ala Ser Asp Ala Ser Ala Val Ile Glu His Thr  
 275 280 285  
 Asn Arg Val Ile Phe Leu Glu Asp Asp Asp Val Ala Ala Val Val Asp  
 290 295 300  
 Gly Arg Leu Ser Ile His Arg Ile Lys Arg Thr Ala Gly His His His  
 305 310 315 320  
 His His His Asp His Pro Gly Arg Ala Val Gln Thr Leu Gln Met Glu  
 325 330 335  
 Leu Gln Gln Ile Met Lys Gly Asn Phe Ser Ser Phe Met Gln Lys Glu  
 340 345 350  
 Ile Phe Glu Gln Pro Glu Ser Val Val Asn Thr Met Arg Gly Arg Val  
 355 360 365  
 Asn Phe Asp Asp Tyr Thr Val Asn Leu Gly Gly Leu Lys Asp His Ile  
 370 375 380  
 Lys Glu Ile Gln Arg Cys Arg Arg Leu Ile Leu Ile Ala Cys Gly Thr  
 385 390 395 400  
 Ser Tyr His Ala Gly Val Ala Thr Arg Gln Val Leu Glu Glu Leu Thr  
 405 410 415  
 Glu Leu Pro Val Met Val Glu Leu Ala Ser Asp Phe Leu Asp Arg Asn  
 420 425 430  
 Thr Pro Val Phe Arg Asp Asp Val Cys Phe Phe Leu Ser Gln Ser Gly  
 435 440 445  
 Glu Thr Ala Asp Thr Leu Met Gly Leu Arg Tyr Cys Lys Glu Arg Gly  
 450 455 460  
 Ala Leu Thr Val Gly Ile Thr Asn Thr Val Gly Ser Ser Ile Ser Arg  
 465 470 475 480  
 Glu Thr Asp Cys Gly Val His Ile Asn Ala Gly Pro Glu Ile Gly Val  
 485 490 495  
 Ala Ser Thr Lys Ala Tyr Thr Ser Gln Phe Val Ser Leu Val Met Phe  
 500 505 510  
 Ala Leu Met Met Cys Asp Asp Arg Ile Ser Met Gln Glu Arg Arg Lys  
 515 520 525  
 Glu Ile Met Leu Gly Leu Lys Arg Leu Pro Asp Leu Ile Lys Glu Val  
 530 535 540  
 Leu Ser Met Asp Asp Glu Ile Gln Lys Leu Ala Thr Glu Leu Tyr His  
 545 550 555 560

Gln	Lys	Ser	Val	Leu	Ile	Met	Gly	Arg	Gly	Tyr	His	Tyr	Ala	Thr	Cys	
				565					570					575		
Leu	Glu	Gly	Ala	Leu	Lys	Ile	Lys	Glu	Ile	Thr	Tyr	Met	His	Ser	Glu	
				580					585					590		
Gly	Ile	Leu	Ala	Gly	Glu	Leu	Lys	His	Gly	Pro	Leu	Ala	Leu	Val	Asp	
				595					600					605		
Lys	Leu	Met	Pro	Val	Ile	Met	Ile	Ile	Met	Arg	Asp	His	Thr	Tyr	Ala	
				610					615					620		
Lys	Cys	Gln	Asn	Ala	Leu	Gln	Gln	Val	Val	Ala	Arg	Gln	Gly	Arg	Pro	
				625					630					635		
Val	Val	Ile	Cys	Asp	Lys	Glu	Asp	Thr	Glu	Thr	Ile	Lys	Asn	Thr	Lys	
				645					650					655		
Arg	Thr	Ile	Lys	Val	Pro	His	Ser	Val	Asp	Cys	Leu	Gln	Gly	Ile	Leu	
				660					665					670		
Ser	Val	Ile	Pro	Leu	Gln	Leu	Leu	Ala	Phe	His	Leu	Ala	Val	Leu	Arg	
				675					680					685		
Gly	Tyr	Asp	Val	Asp	Phe	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	
				690					695					700		
Glu																
705																

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<210> 13
<211> 608
<212> PRT
<213> Escherichia coli
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<400>	13															
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Leu	Glu	Gly	Leu	Arg	Arg	Leu	Glu	Tyr	Arg	Gly	Tyr	Asp	Ser	Ala	Gly	
			20					25					30			
Leu	Ala	Val	Val	Asp	Ala	Glu	Gly	His	Met	Thr	Arg	Leu	Arg	Arg	Leu	
		35					40					45				
Gly	Lys	Val	Gln	Met	Leu	Ala	Gln	Ala	Ala	Glu	Glu	His	Pro	Leu	His	
	50					55					60					
Gly	Gly	Thr	Gly	Ile	Ala	His	Thr	Arg	Trp	Ala	Thr	His	Gly	Glu	Pro	
65					70					75					80	
Ser	Glu	Val	Asn	Ala	His	Pro	His	Val	Ser	Glu	His	Ile	Val	Val	Val	
				85					90					95		
His	Asn	Gly	Ile	Ile	Glu	Asn	His	Glu	Pro	Leu	Arg	Glu	Glu	Leu	Lys	
			100					105					110			
Ala	Arg	Gly	Tyr	Thr	Phe	Val	Ser	Glu	Thr	Asp	Thr	Glu	Val	Ile	Ala	
		115					120					125				

His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu Ala  
 130 135 140  
 Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val Ile  
 145 150 155 160  
 Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly Ser  
 165 170 175  
 Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser Asp  
 180 185 190  
 Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu Glu  
 195 200 205  
 Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp Lys  
 210 215 220  
 Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln Tyr  
 225 230 235 240  
 Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu Ile  
 245 250 255  
 Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile Ser  
 260 265 270  
 His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu Leu  
 275 280 285  
 Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser Tyr  
 290 295 300  
 Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly Ile  
 305 310 315 320  
 Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser Ala  
 325 330 335  
 Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu Thr  
 340 345 350  
 Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr Leu  
 355 360 365  
 Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg Glu  
 370 375 380  
 Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val Ala  
 385 390 395 400  
 Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu Val  
 405 410 415  
 Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His Asp  
 420 425 430  
 Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met Leu  
 435 440 445  
 Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp Lys

450	455	460
His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala Leu 465 470 475 480		
Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu Ala 485 490 495		
Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp Ala 500 505 510		
Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu Lys 515 520 525		
Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu Tyr 530 535 540		
Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met His 545 550 555 560		
Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe Tyr 565 570 575		
Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys Gly 580 585 590		
Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu 595 600 605		

<210> 14  
 <211> 72  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Primer

<400> 14  
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 tcaccccgga cg 72

<210> 15  
 <211> 44  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Primer

<400> 15  
 caaagttgac tottctcttc attgtgttca cgacagactc tggc 44

<210> 16  
 <211> 43  
 <212> DNA  
 <213> Artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 16

aatctagatt catgctcgag cggccgccag tgtgattgat atc

43

&lt;210&gt; 17

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 17

atttttatca gagcgctggg ggtggctatt gacagg

36

&lt;210&gt; 18

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; FLAG tag

&lt;400&gt; 18

Asp Thr Lys Asp Asp Asp Asp Lys

1

5

&lt;210&gt; 19

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; hexa-histidine tag

&lt;400&gt; 19

His His His His His His

1

5